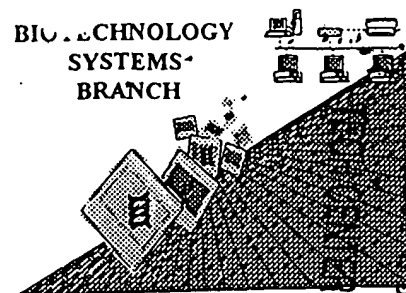


1644

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: us/09/350401

Source: AU 1600

Date Processed by STIC: 10/17/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/350401
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Input field 160 did not match output
See Enclosures/Attachments

1600

RAW SEQUENCE LISTING

DATE: 09/27/2001

PATENT APPLICATION: US/09/350,401

TIME: 14:19:41

Input Set : A:\139_10 SEQLIST.TXT

Output Set: N:\CRF3\09272001\I350401.raw

4 <110> APPLICANT: Alessandro Sette
5 John Sidney
6 Scott Southwood
7 Maria A. Vitiello
8 Brian D. Livingston
9 Esteban Celis
10 Ralph T. Kubo
11 Howard M. Grey
12 Robert Chesnut
14 <120> TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO
15 HEPATITIS B VIRUS USING PEPTIDE AND NUCLEIC ACID
16 COMPOSITIONS
18 <130> FILE REFERENCE: 139.10 US
20 <140> CURRENT APPLICATION NUMBER: US 09/350,401
21 <141> CURRENT FILING DATE: 1999-07-08
23 <150> PRIOR APPLICATION NUMBER: US 08/820,360
24 <151> PRIOR FILING DATE: 1997-03-12
26 <150> PRIOR APPLICATION NUMBER: US 60/013,363
27 <151> PRIOR FILING DATE: 1996-03-13
29 <150> PRIOR APPLICATION NUMBER: US 09/189,702
30 <151> PRIOR FILING DATE: 1998-11-10
32 <150> PRIOR APPLICATION NUMBER: US 08/205,713
33 <151> PRIOR FILING DATE: 1994-03-04
35 <150> PRIOR APPLICATION NUMBER: US 08/159,184
36 <151> PRIOR FILING DATE: 1993-11-29
38 <150> PRIOR APPLICATION NUMBER: US 08/073,205
39 <151> PRIOR FILING DATE: 1993-07-04
E--> 41 <160> NUMBER OF SEQ ID NOS: 3876
43 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Errored
Input 3876 Found 3877

ERRORED SEQUENCES

check diskette for actual contents MH

Does Not Comply
Corrected Diskette Needed

VERIFICATION SUMMARY

DATE: 09/27/2001

PATENT APPLICATION: US/09/350,401

TIME: 14:19:50

Input Set : A:\139_10 SEQLIST.TXT

Output Set: N:\CRF3\09272001\I350401.raw

L:15599 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1197) SEQUENCE:
L:42602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3274
L:42619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3275
L:43130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3314
L:43147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3315
L:43164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3316
L:43181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3317
L:43198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3318
L:43215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3319
L:43232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3320
L:43249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3321
L:43266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3322
L:43283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3323
L:43300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3324
L:43317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3325
L:43334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3326
L:43351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3327
L:43368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3328
L:43385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3329
L:43402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3330
L:43419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3331
L:44073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3381
L:44090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3382
L:44536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3416
L:44553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3417
L:44572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3418
L:44589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3419
L:44606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3420
L:44623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3421
L:44640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3422
L:44657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3423
L:44674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3424
L:44691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3425
L:44708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3426
L:44725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3427
L:44742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3428
L:44759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3429
L:44776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3430
L:44793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3431
L:44810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3432
L:44827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3433
L:50630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3877
L:41 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (3876) Counted (3877)

Attach Printout
Explaining Errors

US/09/350401

<210> 3877
<211> 13
<212> PRT
<213> Artificial Sequence

Input: 3876 sequences
Found: 3877 sequences
Actual file contents as of

10/17/01

MH

<220>
<223> Artificial Peptide

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = cyclohexylalanine, Phe or Tyr

<400> 3877
Ala Lys Xaa Val Trp Ala Asn Thr Leu Lys Ala Ala Ala
1 5 10

Does Not Comply
Corrected Diskette Needed